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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Dec 28 20:25:28 1999; MasPar time 603.24 Seconds 1002.380 Million cell updates/sec

Tabular output not generated.

Title: >US-09-327-230-1 (1-2822) from US09327230.seq 2822

Description:
Perfect Score:
N.A. Sequence:
Comp: 1 gcaacgcacacagacaggca......ttccaggttttgggttttcggg 2822 cgttgcgtgtgtctgtccgt.....aaggtccaaacccaaagccc

Scoring table: TABLE default Gap 6

Nmatch STD:

Searched: 271905 seqs, 107135622 bases N

Dbase 0; Query 0

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

n-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part24 35:part35 36:part36 37:part37 38:part38
39:part39 40:part40 41:part41 42:part42 43:part44
45:part44 45:part45 46:part46 47:part47 48:part48
49:part49 50:part50 51:part51 52:part52 53:part53
54:part49 50:part55 56:part56 57:part57 58:part58
59:part59 60:part60

Statistics: Mean 9.803; Variance 6.092; scale 1.609

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Query Match Length DB	DB		Description	Pred. No
1	2822	100.0	2822	51	V57302	Maize cell death supp	0.00e+00
2	49	1.7		Н	N81164	Base substituted E.co	5.71e-13
ω	44	1.6		9	Q51746	Oligonucleotide probe	3.73e-10
c 4	42	1.5		9	Q51746	Oligonucleotide probe	4.74e-09
c 5	42	1.5		ш	N81164	Base substituted E.co	4.74e-09
6	ω ω	1.2		46	V44650	Mammalian DNA replica	2.82e-04
c 7	34	1.2	91	46	V44650	Mammalian DNA replica	8.68e-05
80	34	1.2		12	Q70467		8.68e-05
9	ω			Š	T76363		2.82e-04

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25	25	25	25	26	26	25	25	26	25	26	26	26	26	29	27	27	29	27	29	29	29	29	28	29	29	27	30	3 <u>1</u>	30	30	3 <u>1</u>	31	32	
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NA probe 26 detects	lori secreted o	i secreted c	endothelin-1	ascular cell	DNA sequenc	ē	TSAR library	Y746	TSAR library	ugate formed k	enger RNA prim	nucleotide tag	er used in th	ze cell death sup	nerate FMN reduc	tance P antiso	leukotriene (ase antis	eneric DNA sequenc	ric DNA s	ric DNA s	eneric DNA sequenc	eneric DNA sequenc	eneric DNA sequenc	ic DNA sequenc	er used in the	n endothelin-1 a	uman interleukin 8	C DNA s	Generic DNA sequence	DNA s		Generic DNA sequence	1
2.05e+00	.05e+0	.05e+0	.05e+0	.18e-0	.18e	.05e+0	.05e+0	.18e-	.05e	.18e-	.18e-	.18e-	.18e-	.74e-	.46e-	.46e-	.74e-	.46e-	.74e-	.74e-	.74e-	.74e-	.29e-	2.74e-02	.74e-	.46e-	.93e-	.86e-	.93e-	.93e-	.86e-	.86e-	.05e-	

ALIGNMENTS

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Novel promoter sequences are provided for the expression of genes in plants. A chimeric gene comprising the promoter operably linked with a heterologous coding sequence is claimed, as are a	resistance, enhancing cell transformation efficiency, engineering herbicide resistance and genetically targeting cell ablations.	LLS1 protein and nucleic acids are useful for activating disease	compositions for suppressing cell death and controlling disease	during photosynthesis. The invention relates to methods and	gene encodes a novel maize protein (see W79001) which inhibits the spread of cell death from wounding or internal stresses that occur	maize leaf spot-1 (11s1) gene (see V57301 and V57303). The 11s1	This nucleotide sequence comprises the promoter region of the	engineering nerbicide resistance or targetting cell ablations Claim 38; Page 51-53: 95mp; English.	activating disease resistance, enhancing transformation efficiency,	New isolated plant cell death suppressing gene - used for e.g.	WPI; 98-506354/43.		UNIV MISSOURI.	(PION-) PIONEER HI-BRED INT INC.		03-MAR-1998; U04040.	11-SEP-1998.	WO9839422-A1.	Zea mays.	âs.	herbicide resistance; dioxygenase		മ	11-JAN-1999 (first entry)	••	LT 1 V57302 standard; DNA; 2822 BP.

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Base substituted E.coli beta-galactosidase alpha-fragment.
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Random point mutations were introduced into the alpha fragment of E.coli, beta-galactosidase. The wild type sequence was obtained as a consider stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which occurred singularly in any given mutant.

See also P80575.

Sequence 204 BP; 21 A; 47 C; 17 G; 11 T; 108 Others;
                                                                          Query Match
Best Local
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Best Local
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Q51746;
31-MAY-1994
                                                                                                                                                                                                                                                                                                                  Synthetic.
EP-571911-A.
01-DEC-1993.
24-MAY-1993; 1
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Lehtovaara P. Knowles J. Koivula A. Bamford J. R.

WPI; 88-279927/40.

Introducing random point mutations into nucleic
by prepn of single stranded template, annealing

"'''normoration, completion of molecules and so
      2209
                                                                                                                   Claim 3; Page 14; 23pp; English.
Oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacteria tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.
Sequence 91 BP; 5 A; 17 C; 15 G; 4 T;
                                                                                                                                                                                                                                       Shank DD, Spears PA;
WPI; 93-378844/48.
New oligo:nucleotide probes specific for Mycobacteria -
detection and amplification of Mycobacteria nucleic ack
                                                                                                                                                                                                                                                                                                                                                                                                ss.
                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide probe MKI4-A Oligonucleotide; DNA probe;
                             13 vhsyyvvhvvshhhsvhhvvhhvhvsvvvvhhvvhvvhhvhyhvyvsvctca
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cottcoccgcccttcctcccttccctgccgtgacgcaaccacactgcgctca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         actattgtgtttggcttcataaaaacacatacaccctattaaattagtataaaaatat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cycgaayycdchvgccgymrttthhyrrmrbnvyrdynrsdaaawyccyrrsvkydccyn 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                            Similarity
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18; Conser
                                                               4.
                                                                                                                                                                                                                                                                                                                     ; 108325.
; US-889651.
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llarity 15.4%;
Conservative
                                                                            1.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91
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                                                                            Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                              mycobacteria;
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Pred. No. 5.71e-13;
58; Mismatches 41
                                                              44;
                                                            Mismatches
                                                                          DB 9; Lo
3.73e-10;
                                                                                                                                                                                                                                                                                                                                                                                                              disease
                                                                                          Length
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RESULT
ID QUAC
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DT 31

Q51746 stand Q51746; 31-MAY-1994

standard;

cDNA;

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Staclosure; p; English.

C Random point mutations were introduced into the alpha fragment of E.coli beta-galactosidase. The wild type sequence was obtained as a single stranded template and an oligonucleotide was hybridised to it to generate a popn of DNA molecules which terminate at all possible nucleotide positions within a specified region. The variable 3' ends generated in this way are used as primers for reverse transcriptase. Nucleotides are misincorporated by the transcriptase and the molecules are completed to forms that can be amplified and then expressed in a suitable host-vector system.

The sequence covers all 176 difft base substitutions, most of which coccurred singularly in any given mutant.
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01-DEC-1993:
24-MAY-1993: 108325:
26-MAY-1992: US-889651.
(BECT ) BECTON DICKINSON C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 14; 23pp; English.

Claim 3; Page 14; 23pp; English.

Oligonucleotide probe MK14-A consists of nucleotides 5-95 of oligonucleotide probe MK14-A consists of nucleotides 5-95 of (Q51735). It hybridized to all spp. of mycobacterial tested, cross reacted to a few non-mycobacterial spp. The probe may be useful as an initial screen for mycobacterial infection. See also Q51735-45 and Q51747-59.

Sequence 91 Bp; 5 A; 17 C; 15 G; 4 T;
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Lehtovaara P. Knowles J.
WPI; 88-279927/40.
                                                                                                                                                                                                                                                                                                              30-MAR-1988;
03-APR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Base substituted
E.coli beta galad
Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-NOV-1990 (first entry)
Base substituted E.coli beta-galactosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New oligo:nucleotide probes detection and amplification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cgssvhsyyvvhvvshhhsvhhvvhvhvhvvhhvvhvvhhvhyhvyvsvctcaagcc 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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                       singularly
P80575.
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ilarity 18.1%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 19..69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA probe; mycobacteria; disease diagnosis;
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Pred. No. 4.74e-
44; Mismatches
                                                                                                                                                                                                                      template, annealing a primer, elongation, of molecules and screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specific for Mycobacteria - of Mycobacteria nucleic acid
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                                                                                                                                                                                                                                                                                  Bamford
      17
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4.74e-09;
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base substitutions;
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      11
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      Τ,
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d in
      Others;
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SEASE

06-OCT-1998 (first entry)
Mammalian DNA replication original bunk replication origin; human;

origin

consensus

sequence,

uniorsconsensus

V44650 standard; DNA; 91 V44650;

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Best Local :
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                                                                                                                                                                                                                                                                                 consensus sequences of the invention, designated uniorsconsensus.

Administration of the consensus sequence or an anti-gene (comprising a double stranded copy of the consensus) is used to inhibit DNA replication in vivo or in vitro. The consensus sequences can also be inserted into an expression vector, used subsequently for in vitro transfection of mammalian cells, to control initiation of DNA replication. They can also be used used to maintain circular plasmids that are capable of semi-conservative replication in proliferating mammalian cells, or inserted into mammalian or human artificial chromosome vectors for gene therapy. Particularly, they are used to create shuttle vector constructs for defining the essential mammalian elements required for maintenance of chromosomal function. The consensus sequence can be combined with cloned numan telomeres and large centromeric blocks for assembly of human artificial chromosomal description of maintenance of the consensus sequence can be combined with cloned between the consensus sequence can be combined with cloned artificial chromosome.
                                                                       1509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-JUN-1998.
12-DEC-1997; CAO972.
21-MAY-1997; US-047322.
16-DEC-1996; US-033374.
(UYMC-) UNIV McGILL.
Cossons NH, Nielsen TO, Price GB, Zannis-Hadjopoulos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 42; 54pp; English.
This sequence represents a human or mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2324
                                                                                                                                                                                                                                                                        artificial chromosomes and maintained as bacterial plasmids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               replication, maintaining circular plasmids artificial chromosomes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human or mammalian origin of replication consensus sequences inhibiting DNA replication, for controlling initiation of
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                                   68 kawsdatakwwwkdakwkmwrkt 90
                                                                                                        8 krawrwwkkdavwwgakrwwkwvwhrassacmdwkaaktwkggwtwarrywkgrkmwwtw 67
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tgtcgacttattttatagttagt
                                                                   taaactattacggataaatagcatgactaccttagtatttaaatgatatcagttgaaata
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                                                                                                                                                               Similarity
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llarity 15.1%;
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10.8%;
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                                                                                                                                          Score 33;
Pred. No.
49; Misma
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Pred.
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                                                                                                                                                               DB 46;
2.82e-04;
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. 4.74e-09;
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CC This sequence represents a human or mammalian DNA replication origin CC consensus sequences of the invention, designated uniorsconsensus.

CC Administration of the consensus sequence or an anti-gene (comprising a double stranded copy of the consensus) is used to inhibit DNA replication or in vivo or in vitto. The consensus sequences can also be inserted into an CC expression vector, used subsequently for in vitro transfection of CC mammalian cells, to control initiation of DNA replication. They can also be used used to maintain circular plasmids that are capable of CC be used used to maintain or human artificial chromosome vectors for gene conservative replication in proliferating mammalian cells, or inserted into mammalian or human artificial chromosome vector constructs for defining the essential mammalian elements required for maintenance of chromosomal function. The consensus sequence can be combined with cloned thuman telomeres and large centromeric blocks for assembly of human construction. The consensus sequence as plasmids, circular or artificial chromosomes and maintained as bacterial plasmids, circular or assembly or as episomal
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Best Local
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  W09418318-A.
18-AUG-1994: U00977.
01-FEB-1994: US-013416.
30-DEC-1993; US-176500.
31-JAN.1994; US-189331.
(UYNC-) UNIV NORTH CAROLIFOWLKES DM, KAY EK;
P-PSDB; R65153.
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070467;
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Cossons NH, Nielsen TO, Price GB,
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gene therapy;
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; US-033374.
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llarity 11.5%;
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sequence of 6, 9 or 12 nucleotides (see
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CO ther specific peptides generated by these generic sequences are shown in 070466-88.

CO ther specific peptides generated by these generic sequences are shown in 070466-88.

CO comprising at least two functional regions - a binding domain with a finity for a ligand and a second effector peptide portion that is comprising at least two functional regions - a binding domain with comprising a ligand and a second effector peptide portion that is commically or biologically active. They may further comprise a linker peptide between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the unpredicted or variant residues. These residues confer some degree of conformational rigidity to the peptides. The TSARs or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, cradicisotope, peptide toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. metal or polyclonal antibodies and therefore circumvent the need for composition of physically active moietical regions.
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Metzger WJ, Nyce JW:

WPI; 97-05127
A method for treating airway disease in a subject has been produced, which involves the topical administration of an essentially adenosine free antisense oligonucleotide (ON) to the airway epithelium of the subject. The present sequence is an antisense oligonucleotide specific for the human interleukin 8, targeted at the initiation codon. The method can be used to treat airway diseases such as cystic fibrosis, asthma, chronic obstructive pulmonary disease, bronchitis and other airway diseases characterised by an inflammatory response. By eliminating adenosine from the antisense on, its liberation upon antisense degradation is prevented, thereby preventing adenosine-induced bronchoconstriction in patients with hyper-reactive airways. Sequence 172 BP; 0 A; 35 C; 42 G; 39 T;
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                                                                                                                                                                                                                                                                                                                                                                                          Claim 5;
A method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treatment of airway diseases such as asthma - by topically applying adenosine-free antisense oligo:nucleotide to airway epithelium of
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06-JUN-1996; U09306
07-JUN-1995; US-474
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W09640162-A1.
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interleukin 8 antisense oligonucleotide.
a; airway epithelium; adenosine free; cystic fibrosis;
a; airway entre monary disease; bronchitis; ss.
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                                                                                                                                                                                                                          PT Identifying proteins or peptide(s) which bind a ligand - by recemning a recombinant vector library expressing fusion proteins processing a binding domain and an effector domain proteins processing a binding domain and an effector domain proteins processing a binding domain and an effector domain proteins processing the proteins processed and an effector domain proteins processed and proteins proteins or peptides. This generate random TSAR (Totally CO 970465 is a generic DNA sequence used to generate random TSAR (Totally CS 970465 is a generic DNA sequence used to generic formula can also be created as follows: x (NNB)6(TGC)(NNB)112(NNB)44(TGC)(NNB)31 x x constant the specific peptides generic sequences are shown in Q70466-68. Confer specific peptides generated by these generic sequences are shown in CR 65151-54. TSARS are concatenated heterofunctional proteins or peptides, comprising at least two functional regions - a binding domain with CC affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker operated between the 2 domains. The oligonucleotides are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned confer some degree of conformational rigidity to the peptides. The TSARS CC or compsns. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, cradicistope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. consocional or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody continued activity allowing direct and rapid detection in a screening process. Sequence 114 BP; 0 A; 2 C; 2 G; 2 T;
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Q70465;
05-APR-1995 (fir
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30-DEC-1993;
31-JAN-1994;
        1109
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les 4; Conse
                                                                 ω
     gcattgttcccaatcgtcctctgcgcatgctggttcccacgtgtattttcctcgcgcgca
                                                              tccgccacggcccacgggtgggttcgtgtcgttctcaccgccggtcaatctcccctccgc 2108
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31; Conser
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US-013416.
US-176500.
US-189331.
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larity 31.3%;
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sequence of 6, 9 or 12 nucleotides
comments)"
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32; M
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9.05e-04;
76;
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2.82e-04;
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Q70468 standard;
Q70468;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYNC-) UNIV NORTH CAROLINA Fowlkes DM, Kay BK; WPI; 94-279739/34.
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30-DEC-1993;
                                                           63 bnnbnnbnnbnnbnnbtgcnnbnnbnnbnnbnnbnnbnnbnnbnnbnnb
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comments)"
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/** note= This sequence represents 'Z
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                                                                                                                                                                                                                                                                                                              В
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CC 070469 is a generic DNA sequence used to generate random TSAR peptide of this generic formula can be represented as follows: x(TGC)(NNB)10-CC (TGC)(NNB)52(NNB)14(TGC)Y. X and Y are flanking restriction of the same as Y) that are not specified further. This considers (X is not the same as Y) that are cloverleaf in structure. Other generic sequences are shown in 070465-68. Other specific peptides of the sequences are shown in R65150-54. TSARs are concatenated by these generic sequences are shown in R65150-54. TSARs are concatenated between concitional proteins or peptides, comprising at least the sequences are abinding domain with affinity for a ligand and concatenated between the peptide sequences are also designed so that the expressed peptide contains 2 or 4 cysteine residues positioned in, or flanking, the conformational rigidity to the peptides. The TSARs or compans. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, sequences are light to the peptides. The TSARs or compans.
                                                                                                                                                                                                                                                                                                                                                    Matches
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30-DEC-1993; US-176500.
31-JAN-1994; US-189331.
(UYNC-) UNIV NORTH CAROLINA.
FOWLKES DM, KAY BK;
WPI; 94-279739/34.
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18-AUG-1994.
01-FEB-1994;
01-FEB-1993;
30-DEC-1993;
31-JAN-1994;
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                Generic DNA sequence to generate a random TSAR peptide library. TSAR; totally synthetic affinity reagent; synthetic; binding do effector domain; concatenated heterofunctional protein; linker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             formation or in vivo antibody production. The TSARs are easil characterised and have designed activity allowing direct and
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Synthetic.
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Generic DNA sequence
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Q70470 standard;
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llarity 3.7%;
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Synthetic affinity reagent; synthetic; binding do
in; concateneated heterofunctional protein; linker
; detection; screening; treatment; generic; ss.
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screening; treatment;
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Pred. No. 2.86e:
31; Mismatches
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nucleotides
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01-FEB-1994;
01-FEB-1993;
30-DEC-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       heterofunctional proteins or peptides, comprising at least two functions regions - a binding domain with affinity for a ligand and a second effector peptide portion that is chemically or biologically active. They may further comprise a linker peptide between the 2 domains. The TSARs or compans. comprising a TSAR binding domain can be used in vivo to deliver a chemically or biologically active moiety, eg. metal ion, radioisotope, peptide, toxin or enzyme, to the specific target or on the cell. They can also replace the function of macromolecules, eg. monoclonal or polyclonal antibodies and therefore circumvent the need for complex methods of hybridoma formation or in vivo antibody production. The TSARs are easily characterised and have designed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYNC-) UNIV NO Fowlkes DM, Ka WPI; 94-279739/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion proteins comprising a binding domain and an effector domain Disclosure; Page 36; 255pp; English.

Q70470 is a generic DNA sequence used to generate random TSAR (Totally Synthetic Affinity Reagents) peptides. This generic formula can also be represented as follows: X(NNB)4(CAC)(NNB)4(CAC)(NNB)8Z(NNB)6(CAC)(NNB)8
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                                                                                                                                                                                Generic DNA sequence to generate a random TSAR petide library. TSAR; totally synthetic affinity reagent; synthetic; binding of effector domain; concateneated heterofunctional protein; linke direct; rapid; detection; screening; treatment; generic; ss.
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Q70465 standard;
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; US-189331.
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larity 5.8%;
Conservative
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sequence of 6, 9 or 12 nucleotides (se
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A; 10 C;
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Pred. No.
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29; N
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ches 68;
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CC Q70465 is a generic DNA sequence used to generate random TSAR (Totally CC Synthetic Affinity Reagents) peptides. This generic formula can also be CC and Y are flanking restriction sites (X is not the same as Y) that are CC and Y are flanking restriction sites (X is not the same as Y) that are CC other specified further. Other generic sequences are shown in Q70466-68. CC omprising at least two functional regions - a binding domain with CC chemically or biologically active. They may further comprise a linker CC chemically or biologically active. They may further comprise a linker CC comprising at least two functional regions - a binding domain with CC chemically or biologically active. They may further comprise a linker CC chemically or biologically active. They may further comprise a linker CC comprising a TSAR binding domain residues. These residues confer some degree of conformational rigidity to the peptides. The CC deliver a chemically or biologically active moiety, eg. metal ion, CC deliver a chemically or biologically active moiety, eg. metal ion, CC call. They can also replace the function of macromoleules, eg.

CC monoclonal or polycional antibodies and therefore circumvent the need CC cell. They can also replace the function of macromoleules, eg.

CC monoclonal or The TSARs are easily characterised and have designed CC activity allowing direct and rapid detection in a screening process. Squence 114 BP; 0 A; 2 C; 2 G; 2 T;
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Best Local
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                                                                                                 WO9418318-A.
18-AUG-1994; U00977.
01-FEB-1994; US-013416.
01-FEB-1993; US-176500.
31-JAN-1994; US-189331.
(UXNC-) UNIV NORTH CAROLINA.
FOWLKES DM, KAY BK;
WPI; 94-279739/34.
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(UYNC-) UNIV NORTH (
Fowlkes DM, Kay BK,
WPI; 94-279739/34.
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      Identifying proteins or peptide(s) which bind a ligand - by screening a recombinant vector library expressing fusion procomprising a binding domain and an effector domain
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28; N
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Disclosure; Page 35; 255pp; English.

CO (70466) is a generic DNA sequence used to generate random TSAR peptide
CC This generic formula can be represented as follows: X(TGC)(NNB)10.

CC (TGC)(NNB)2(TGC)(NNB)14(TGC)Y. X and Y are flanking restriction
CC sites (X is not the same as Y) that are not specified further. This
CC sequence generates peptides that are cloverleaf in structure. Other
CC generate by these generic sequences are shown in R65150-54. TSARs are
CC concatenated heterofunctional proteins or peptides, comprising at least
CC two functional regions - a binding domain with affinity for a ligand and
CC a second effector peptide portion that is chemically or biologically
CC active. They may further comprise a linker peptide between the 2 domains.
CC The oligonucleotides are also designed so that the expressed peptide
CC contains 2 or 4 cysteine residues positioned in, or flanking, the
CC conformational rigidity to the peptides. These residues confer some degree of
CC conformational rigidity to the peptides. The TSARs or compsis. comprising
CC a TSAR binding domain can be used in vivo to deliver a chemically or
CC or enzyme, to the specific target or on the cell. They can also replace
CC the function of macromolecules, eg. monoclonal or polyclonal antibodies
CC and therefore circumvent the need for complex methods of hybridoma
CC characterised and have designed activity allowing direct and rapid
CC characterised and have designed activity allowing direct and rapid
CC detection in a screening process.
SO Sequence 114 BP; 0 A; 4 C; 4 G; 4 T;

COUNTY Match
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- Cp 2117 ttgcgccgcgcgggggggggattgaccggcggtgagaacgaccgaac 2070

Search completed: Tue Dec 28 20:54:38 1999 Job time: 1750 secs.